

SEQUENCE LISTING

(1) GENERAL INFORMATION:

5 (i) APPLICANT: Ashkenazi, Avi J.
Baker, Kevin
Gurney, Austin
Wood, William

10 (ii) TITLE OF INVENTION: Apo-2DcR

(iii) NUMBER OF SEQUENCES: 13

(iv) CORRESPONDENCE ADDRESS:

- (A) ADDRESSEE: Genentech, Inc.
(B) STREET: 460 Point San Bruno Blvd
(C) CITY: South San Francisco
(D) STATE: California
(E) COUNTRY: USA
(F) ZIP: 94080

(v) COMPUTER READABLE FORM:

- (A) MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
(B) COMPUTER: IBM PC compatible
(C) OPERATING SYSTEM: PC-DOS/MS-DOS
(D) SOFTWARE: WinPatin (Genentech)

(vi) CURRENT APPLICATION DATA:

- (A) APPLICATION NUMBER:
(B) FILING DATE: 18-Jun-1997
(C) CLASSIFICATION:

(viii) ATTORNEY/AGENT INFORMATION:

- (A) NAME: Marschang, Diane L.
(B) REGISTRATION NUMBER: 35,600

(C) REFERENCE/DOCKET NUMBER: P1110

(ix) TELECOMMUNICATION INFORMATION:

(A) TELEPHONE: 415/225-5416

5 (B) TELEFAX: 415/952-9881

(C) TELEX: 910/371-7168

(2) INFORMATION FOR SEQ ID NO:1:

10 (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 259 amino acids

(B) TYPE: Amino Acid

(D) TOPOLOGY: Linear

15 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

Met Ala Arg Ile Pro Lys Thr Leu Lys Phe Val Val Val Ile Val
1 5 10 15

20 Ala Val Leu Leu Pro Val Leu Ala Tyr Ser Ala Thr Thr Ala Arg
20 25 30

25 Gln Glu Glu Val Pro Gln Gln Thr Val Ala Pro Gln Gln Gln Arg
35 40 45

His Ser Phe Lys Gly Glu Glu Cys Pro Ala Gly Ser His Arg Ser
50 55 60

30 Glu His Thr Gly Ala Cys Asn Pro Cys Thr Glu Gly Val Asp Tyr
65 70 75

Thr Asn Ala Ser Asn Asn Glu Pro Ser Cys Phe Pro Cys Thr Val
80 85 90

35 Cys Lys Ser Asp Gln Lys His Lys Ser Ser Cys Thr Met Thr Arg

95	100	105
Asp Thr Val Cys Gln Cys Lys Glu Gly Thr Phe Arg Asn Glu Asn		
110	115	120
5		
Ser Pro Glu Met Cys Arg Lys Cys Ser Arg Cys Pro Ser Gly Glu		
125	130	135
Val Gln Val Ser Asn Cys Thr Ser Trp Asp Asp Ile Gln Cys Val		
140	145	150
10		
Glu Glu Phe Gly Ala Asn Ala Thr Val Glu Thr Pro Ala Ala Glu		
155	160	165
15		
Glu Thr Met Asn Thr Ser Pro Gly Thr Pro Ala Pro Ala Ala Glu		
170	175	180
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Glu Thr Met Asn Thr Ser Pro Gly Thr Pro Ala Pro Ala Ala Glu		
185	190	195
25		
Glu Thr Met Thr Thr Ser Pro Gly Thr Pro Ala Pro Ala Ala Glu		
200	205	210
30		
Glu Thr Met Thr Ser Pro Gly Thr Pro Ala Pro Ala Ala Glu		
215	220	225
35		
Glu Thr Met Thr Thr Ser Pro Gly Thr Pro Ala Ser Ser His Tyr		
230	235	240
40		
Leu Ser Cys Thr Ile Val Gly Ile Ile Val Leu Ile Val Leu Leu		
245	250	255
45		
Ile Val Phe Val		
259		

(2) INFORMATION FOR SEQ ID NO:2:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1180 base pairs
 - (B) TYPE: Nucleic Acid
 - (C) STRANDEDNESS: Single
 - (D) TOPOLOGY: Linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

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GCTGTGGGAA CCTCTCCACG CGCACGAACT CAGCCAACGA TTTCTGATAG 50

ATTTTGGA GTTGACCAAG AGATGCAAGG GGTGAAGGGAG CGCTTCCTAC 100

CGTTAGGGAA CTCTGGGGAC AGAGCGCCCC GGCCGCCTGA TGGCCGAGGC 150

AGGGTGCAC CCAGGACCCA GGACGGCGTC GGGAAACCATA CC ATG 195

Met

1

GCC CGG ATC CCC AAG ACC CTA AAG TTC GTC GTC GTC ATC 234

Ala Arg Ile Pro Lys Thr Leu Lys Phe Val Val Val Ile

5 10

25

GTC GCG GTC CTG CTG CCA GTC CTA GCT TAC TCT GCC ACC 273

Val Ala Val Leu Leu Pro Val Leu Ala Tyr Ser Ala Thr

15 20 25

30 ACT GCC CGG CAG GAG GAA GTT CCC CAG CAG ACA GTG GCC 312

Thr Ala Arg Gln Glu Glu Val Pro Gln Gln Thr Val Ala

30 35 40

CCA CAG CAA CAG AGG CAC AGC TTC AAG GGG GAG GAG TGT 351

35 Pro Gln Gln Gln Arg His Ser Phe Lys Gly Glu Glu Cys

	45	50	
	CCA GCA GGA TCT CAT AGA TCA GAA CAT ACT GGA GCC TGT 390		
	Pro Ala Gly Ser His Arg Ser Glu His Thr Gly Ala Cys		
5	55	60	65
	AAC CCG TGC ACA GAG GGT GTG GAT TAC ACC AAC GCT TCC 429		
	Asn Pro Cys Thr Glu Gly Val Asp Tyr Thr Asn Ala Ser		
	70	75	
10			
	AAC AAT GAA CCT TCT TGC TTC CCA TGT ACA GTT TGT AAA 468		
	Asn Asn Glu Pro Ser Cys Phe Pro Cys Thr Val Cys Lys		
	80	85	90
15	TCA GAT CAA AAA CAT AAA AGT TCC TGC ACC ATG ACC AGA 507		
	Ser Asp Gln Lys His Lys Ser Ser Cys Thr Met Thr Arg		
	95	100	105
20	GAC ACA GTG TGT CAG TGT AAA GAA GGC ACC TTC CGG AAT 546		
	Asp Thr Val Cys Gln Cys Lys Glu Gly Thr Phe Arg Asn		
	110	115	
25	GAA AAC TCC CCA GAG ATG TGC CGG AAG TGT AGC AGG TGC 585		
	Glu Asn Ser Pro Glu Met Cys Arg Lys Cys Ser Arg Cys		
	120	125	130
	CCT AGT GGG GAA GTC CAA GTC AGT AAT TGT ACG TCC TGG 624		
	Pro Ser Gly Glu Val Gln Val Ser Asn Cys Thr Ser Trp		
	135	140	
30			
	GAT GAT ATC CAG TGT GTT GAA GAA TTT GGT GCC AAT GCC 663		
	Asp Asp Ile Gln Cys Val Glu Glu Phe Gly Ala Asn Ala		
	145	150	155
35	ACT GTG GAA ACC CCA GCT GCT GAA GAG ACA ATG AAC ACC 702		

Thr Val Glu Thr Pro Ala Ala Glu Glu Thr Met Asn Thr
160 165 170

AGC CCG GGG ACT CCT GCC CCA GCT GCT GAA GAG ACA ATG 741
5 Ser Pro Gly Thr Pro Ala Pro Ala Ala Glu Glu Thr Met
175 180

AAC ACC AGC CCA GGG ACT CCT GCC CCA GCT GCT GAA GAG 780
Asn Thr Ser Pro Gly Thr Pro Ala Pro Ala Ala Glu Glu
10 185 190 195

ACA ATG ACC ACC AGC CCG GGG ACT CCT GCC CCA GCT GCT 819
Thr Met Thr Thr Ser Pro Gly Thr Pro Ala Pro Ala Ala
200 205

GAA GAG ACA ATG ACC ACC AGC CCG GGG ACT CCT GCC CCA 858
Glu Glu Thr Met Thr Ser Pro Gly Thr Pro Ala Pro
210 215 220

GCT GCT GAA GAG ACA ATG ACC ACC AGC CCG GGG ACT CCT 897
Ala Ala Glu Glu Thr Met Thr Thr Ser Pro Gly Thr Pro
225 230 235

GCC TCT TCT CAT TAC CTC TCA TGC ACC ATC GTA GGG ATC 936
Ala Ser Ser His Tyr Leu Ser Cys Thr Ile Val Gly Ile
240 245

ATA GTT CTA ATT GTG CTT CTG ATT GTG TTT GTT T 970
Ile Val Leu Ile Val Leu Leu Ile Val Phe Val
30 250 255 259

GAAAGACTTC ACTGTGGAAG AAATTCCCTTC CTTACCTGAA AGGTTCAGGT 1020

AGGCGCTGGC TGAGGGCGGG GGGCGCTGGA CACTCTCTGC CCTGCCTCCC 1070

TCTGCTGTGT TCCCCACAGAC AGAAAAGCCT GCCCCCTGCC CAAAAAAA 1120

AAAAAAAAAA AAAAAAAAAA AAAAAAAAAA AAAAAAAAAA AAAAAAAAAA 1170

5 AAAAAAAAAA 1180

(2) INFORMATION FOR SEQ ID NO:3:

(i) SEQUENCE CHARACTERISTICS:

- 10 (A) LENGTH: 299 amino acids
(B) TYPE: Amino Acid
(D) TOPOLOGY: Linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

Met Gln Gly Val Lys Glu Arg Phe Leu Pro Leu Gly Asn Ser Gly
-40 -35 -30

Asp Arg Ala Pro Arg Pro Pro Asp Gly Arg Gly Arg Val Arg Pro
-25 -20 -15

Arg Thr Gln Asp Gly Val Gly Asn His Thr Met Ala Arg Ile Pro
-10 -5 1 5

Lys Thr Leu Lys Phe Val Val Val Ile Val Ala Val Leu Leu Pro
10 15 20

Val Leu Ala Tyr Ser Ala Thr Thr Ala Arg Gln Glu Glu Val Pro
25 30 35

30 Gln Gln Thr Val Ala Pro Gln Gln Arg His Ser Phe Lys Gly
40 45 50

Glu Glu Cys Pro Ala Gly Ser His Arg Ser Glu His Thr Gly Ala
35 55 60 65

Cys Asn Pro Cys Thr Glu Gly Val Asp Tyr Thr Asn Ala Ser Asn
70 75 80

Asn Glu Pro Ser Cys Phe Pro Cys Thr Val Cys Lys Ser Asp Gln
5 85 90 95

Lys His Lys Ser Ser Cys Thr Met Thr Arg Asp Thr Val Cys Gln
100 105 110

10 Cys Lys Glu Gly Thr Phe Arg Asn Glu Asn Ser Pro Glu Met Cys
115 120 125

Arg Lys Cys Ser Arg Cys Pro Ser Gly Glu Val Gln Val Ser Asn
130 135 140

Cys Thr Ser Trp Asp Asp Ile Gln Cys Val Glu Glu Phe Gly Ala
145 150 155

Asn Ala Thr Val Glu Thr Pro Ala Ala Glu Glu Thr Met Asn Thr
20 160 165 170

Ser Pro Gly Thr Pro Ala Pro Ala Ala Glu Glu Thr Met Asn Thr
175 180 185

25 Ser Pro Gly Thr Pro Ala Pro Ala Ala Glu Glu Thr Met Thr Thr
190 195 200

Ser Pro Gly Thr Pro Ala Pro Ala Ala Glu Glu Thr Met Thr Thr
30 205 210 215

Ser Pro Gly Thr Pro Ala Pro Ala Ala Glu Glu Thr Met Thr Thr
220 225 230

35 Ser Pro Gly Thr Pro Ala Ser Ser His Tyr Leu Ser Cys Thr Ile
235 240 245

Val Gly Ile Ile Val Leu Ile Val Leu Leu Ile Val Phe Val
250 255 259

(2) INFORMATION FOR SEQ ID NO:4:

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- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 1180 base pairs
 - (B) TYPE: Nucleic Acid
 - (C) STRANDEDNESS: Single
 - (D) TOPOLOGY: Linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

15 GCTGTGGAA CCTCTCCACG CGCACGAACT CAGCCAACGA TTTCTGATAG 50

20 ATTTTTGGGA GTTGACCAAG AG ATG CAA GGG GTG AAG GAG 90
Met Gln Gly Val Lys Glu
-40 -35

25 CGC TTC CTA CCG TTA GGG AAC TCT GGG GAC AGA GCG CCC 129
Arg Phe Leu Pro Leu Gly Asn Ser Gly Asp Arg Ala Pro
-30 -25

30 CGG CCG CCT GAT GGC CGA GGC AGG GTG CGA CCC AGG ACC 168
Arg Pro Pro Asp Gly Arg Gly Arg Val Arg Pro Arg Thr
-20 -15 -10

35 CAG GAC GGC GTC GGG AAC CAT ACC ATG GCC CGG ATC CCC 207
Gln Asp Gly Val Gly Asn His Thr Met Ala Arg Ile Pro
-5 1 5

40 AAG ACC CTA AAG TTC GTC GTC ATC GTC GCG GTC CTG 246
Lys Thr Leu Lys Phe Val Val Val Ile Val Ala Val Leu
35 10 15

CTG CCA GTC CTA GCT TAC TCT GCC ACC ACT GCC CGG CAG 285
 Leu Pro Val Leu Ala Tyr Ser Ala Thr Thr Ala Arg Gln
 20 25 30

5 GAG GAA GTT CCC CAG CAG ACA GTG GCC CCA CAG CAA CAG 324
 Glu Glu Val Pro Gln Gln Thr Val Ala Pro Gln Gln
 35 40

10 AGG CAC AGC TTC AAG GGG GAG GAG TGT CCA GCA GGA TCT 363
 Arg His Ser Phe Lys Gly Glu Glu Cys Pro Ala Gly Ser
 45 50 55

15 CAT AGA TCA GAA CAT ACT GGA GCC TGT AAC CCG TGC ACA 402
 His Arg Ser Glu His Thr Gly Ala Cys Asn Pro Cys Thr
 60 65 70

20 GAG GGT GTG GAT TAC ACC AAC GCT TCC AAC AAT GAA CCT 441
 Glu Gly Val Asp Tyr Thr Asn Ala Ser Asn Asn Glu Pro
 75 80

25 TCT TGC TTC CCA TGT ACA GTT TGT AAA TCA GAT CAA AAA 480
 Ser Cys Phe Pro Cys Thr Val Cys Lys Ser Asp Gln Lys
 85 90 95

30 CAT AAA AGT TCC TGC ACC ATG ACC AGA GAC ACA GTG TGT 519
 His Lys Ser Ser Cys Thr Met Thr Arg Asp Thr Val Cys
 100 105

35 CAG TGT AAA GAA GGC ACC TTC CGG AAT GAA AAC TCC CCA 558
 Gln Cys Lys Glu Gly Thr Phe Arg Asn Glu Asn Ser Pro
 110 115 120

40 GAG ATG TGC CGG AAG TGT AGC AGG TGC CCT AGT GGG GAA 597
 Glu Met Cys Arg Lys Cys Ser Arg Cys Pro Ser Gly Glu
 125 130 135

GTC CAA GTC AGT AAT TGT ACG TCC TGG GAT GAT ATC CAG 636
Val Gln Val Ser Asn Cys Thr Ser Trp Asp Asp Ile Gln
140 145

5 TGT GTT GAA GAA TTT GGT GCC AAT GCC ACT GTG GAA ACC 675
Cys Val Glu Glu Phe Gly Ala Asn Ala Thr Val Glu Thr
150 155 160

10 CCA GCT GCT GAA GAG ACA ATG AAC ACC AGC CCG GGG ACT 714
Pro Ala Ala Glu Glu Thr Met Asn Thr Ser Pro Gly Thr
165 170

15 CCT GCC CCA GCT GCT GAA GAG ACA ATG AAC ACC AGC CCA 753
Pro Ala Pro Ala Ala Glu Glu Thr Met Asn Thr Ser Pro
175 180 185

20 GGG ACT CCT GCC CCA GCT GCT GAA GAG ACA ATG ACC ACC 792
Gly Thr Pro Ala Pro Ala Ala Glu Glu Thr Met Thr Thr
190 195 200

25 AGC CCG GGG ACT CCT GCC CCA GCT GCT GAA GAG ACA ATG 831
Ser Pro Gly Thr Pro Ala Pro Ala Ala Glu Glu Thr Met
205 210

30 ACC ACC AGC CCG GGG ACT CCT GCC CCA GCT GCT GAA GAG 870
Thr Thr Ser Pro Gly Thr Pro Ala Pro Ala Ala Glu Glu
215 220 225

35 ACA ATG ACC ACC AGC CCG GGG ACT CCT GCC TCT TCT CAT 909
Thr Met Thr Ser Pro Gly Thr Pro Ala Ser Ser His
230 235

TAC CTC TCA TGC ACC ATC GTA GGG ATC ATA GTT CTA ATT 948
Tyr Leu Ser Cys Thr Ile Val Gly Ile Ile Val Leu Ile
240 245 250

GTG CTT CTG ATT GTG TTT GTT T GAAAGACTTC ACTGTGGAAG 990
Val Leu Leu Ile Val Phe Val
255 259

5 AAATTCCCTTC CTTACCTGAA AGGTTCAGGT AGGCGCTGGC TGAGGGCGGG 1040
GGGCGCTGGA CACTCTCTGC CCTGCCTCCC TCTGCTGTGT TCCCCACAGAC 1090
10 AGAAAACGCCT GCCCCTGCC CAAAAAAA AAAAAAAA AAAAAAAA 1140
AAAAAAA AAAAAAAA AAAAAAAA AAAAAAAA 1180

(2) INFORMATION FOR SEQ ID NO:5:

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CAGGAAACAG CTATGACCAC CTGCACACCT GCAAATCCAT T 41

(2) INFORMATION FOR SEQ ID NO:7:

5 (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 49 amino acids
- (B) TYPE: Amino Acid
- (D) TOPOLOGY: Linear

10 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:

Cys Arg Glu Cys Glu Ser Gly Ser Phe Thr Ala Ser Glu Asn His
1 5 10 15

15 Leu Arg His Cys Leu Ser Cys Ser Lys Cys Arg Lys Glu Met Gly
20 25 30

20 Gln Val Glu Ile Ser Ser Cys Thr Val Asp Arg Asp Thr Val Cys
35 40 45

25 Gly Cys Arg Lys
49

30 (2) INFORMATION FOR SEQ ID NO:8:

35 (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 48 amino acids
- (B) TYPE: Amino Acid
- (D) TOPOLOGY: Linear

30 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:

35 Cys Asn Pro Cys Thr Glu Gly Val Asp Tyr Thr Asn Ala Ser Asn
1 5 10 15

Asn Glu Pro Ser Cys Phe Pro Cys Thr Val Cys Lys Ser Asp Gln
20 25 30

Lys His Lys Ser Ser Cys Thr Met Thr Arg Asp Thr Val Cys Gln
5 35 40 45

Cys Lys Glu
48

10 (2) INFORMATION FOR SEQ ID NO:9:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 70 base pairs
- (B) TYPE: Nucleic Acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:9:

GGGAGCCGCT CATGAGGAAG TTGGGCCTCA TGGACAATGA GATAAAGGTG 50

GCTAAAGCTG AGGCAGCGGG 70

25 (2) INFORMATION FOR SEQ ID NO:10:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1799 base pairs
- (B) TYPE: Nucleic Acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:10:

CCCACCGCGTC CGCATAAAATC AGCACGCGGC CGGAGAACCC CGCAATCTCT 50

GCGCCCACAA AATACACCGA CGATGCCCGA TCTACTTTAA GGGCTGAAAC 100

5 CCACGGGCCT GAGAGACTAT AAGAGCGTTC CCTACCGCC ATG GAA 145
Met Glu
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CAA CGG GGA CAG AAC GCC CCG GCC GCT TCG GGG GCC CGG 184
10 Gln Arg Gly Gln Asn Ala Pro Ala Ala Ser Gly Ala Arg
5 10 15

AAA AGG CAC GGC CCA GGA CCC AGG GAG GCG CGG GGA GCC 223
Lys Arg His Gly Pro Gly Pro Arg Glu Ala Arg Gly Ala
20 25

AGG CCT GGG CTC CGG GTC CCC AAG ACC CTT GTG CTC GTT 262
Arg Pro Gly Leu Arg Val Pro Lys Thr Leu Val Leu Val
30 35 40

GTC GCC GCG GTC CTG CTG TTG GTC TCA GCT GAG TCT GCT 301
Val Ala Ala Val Leu Leu Leu Val Ser Ala Glu Ser Ala
45 50

25 CTG ATC ACC CAA CAA GAC CTA GCT CCC CAG CAG AGA GCG 340
Leu Ile Thr Gln Gln Asp Leu Ala Pro Gln Gln Arg Ala
55 60 65

30 GCC CCA CAA CAA AAG AGG TCC AGC CCC TCA GAG GGA TTG 379
Ala Pro Gln Gln Lys Arg Ser Ser Pro Ser Glu Gly Leu
70 75 80

TGT CCA CCT GGA CAC CAT ATC TCA GAA GAC GGT AGA GAT 418
Cys Pro Pro Gly His His Ile Ser Glu Asp Gly Arg Asp
35 85 90

TGC ATC TCC TGC AAA TAT GGA CAG GAC TAT AGC ACT CAC 457
 Cys Ile Ser Cys Lys Tyr Gly Gln Asp Tyr Ser Thr His
 95 100 105

5 TGG AAT GAC CTC CTT TTC TGC TTG CGC TGC ACC AGG TGT 496
 Trp Asn Asp Leu Leu Phe Cys Leu Arg Cys Thr Arg Cys
 110 115

10 GAT TCA GGT GAA GTG GAG CTA AGT CCC TGC ACC ACG ACC 535
 Asp Ser Gly Glu Val Glu Leu Ser Pro Cys Thr Thr Thr
 120 125 130

15 AGA AAC ACA GTG TGT CAG TGC GAA GAA GGC ACC TTC CGG 574
 Arg Asn Thr Val Cys Gln Cys Glu Glu Gly Thr Phe Arg
 135 140 145

20 GAA GAA GAT TCT CCT GAG ATG TGC CGG AAG TGC CGC ACA 613
 Glu Glu Asp Ser Pro Glu Met Cys Arg Lys Cys Arg Thr
 150 155

25 GGG TGT CCC AGA GGG ATG GTC AAG GTC GGT GAT TGT ACA 652
 Gly Cys Pro Arg Gly Met Val Lys Val Gly Asp Cys Thr
 160 165 170

30 CCC TGG AGT GAC ATC GAA TGT GTC CAC AAA GAA TCA GGC 691
 Pro Trp Ser Asp Ile Glu Cys Val His Lys Glu Ser Gly
 175 180

35 ATC ATC ATA GGA GTC ACA GTT GCA GCC GTA GTC TTG ATT 730
 Ile Ile Ile Gly Val Thr Val Ala Ala Val Val Leu Ile
 185 190 195

GTG GCT GTG TTT GTT TGC AAG TCT TTA CTG TGG AAG AAA 769
 Val Ala Val Phe Val Cys Lys Ser Leu Leu Trp Lys Lys
 200 205 210

GTC CTT CCT TAC CTG AAA GGC ATC TGC TCA GGT GGT GGT 808
Val Leu Pro Tyr Leu Lys Gly Ile Cys Ser Gly Gly Gly
215 220

5 GGG GAC CCT GAG CGT GTG GAC AGA AGC TCA CAA CGA CCT 847
Gly Asp Pro Glu Arg Val Asp Arg Ser Ser Gln Arg Pro
225 230 235

10 GGG GCT GAG GAC AAT GTC CTC AAT GAG ATC GTG AGT ATC 886
Gly Ala Glu Asp Asn Val Leu Asn Glu Ile Val Ser Ile
240 245

15 TTG CAG CCC ACC CAG GTC CCT GAG CAG GAA ATG GAA GTC 925
Leu Gln Pro Thr Gln Val Pro Glu Gln Glu Met Glu Val
250 255 260

20 CAG GAG CCA GCA GAG CCA ACA GGT GTC AAC ATG TTG TCC 964
Gln Glu Pro Ala Glu Pro Thr Gly Val Asn Met Leu Ser
265 270 275

25 CCC GGG GAG TCA GAG CAT CTG CTG GAA CCG GCA GAA GCT 1003
Pro Gly Glu Ser Glu His Leu Leu Glu Pro Ala Glu Ala
280 285

30 GAA AGG TCT CAG AGG AGG AGG CTG CTG GTT CCA GCA AAT 1042
Glu Arg Ser Gln Arg Arg Arg Leu Leu Val Pro Ala Asn
290 295 300

35 GAA GGT GAT CCC ACT GAG ACT CTG AGA CAG TGC TTC GAT 1081
Glu Gly Asp Pro Thr Glu Thr Leu Arg Gln Cys Phe Asp
305 310

40 GAC TTT GCA GAC TTG GTG CCC TTT GAC TCC TGG GAG CCG 1120
Asp Phe Ala Asp Leu Val Pro Phe Asp Ser Trp Glu Pro
315 320 325

CTC ATG AGG AAG TTG GGC CTC ATG GAC AAT GAG ATA AAG 1159
Leu Met Arg Lys Leu Gly Leu Met Asp Asn Glu Ile Lys
330 335 340

5 GTG GCT AAA GCT GAG GCA GCG GGC CAC AGG GAC ACC TTG 1198
Val Ala Lys Ala Glu Ala Ala Gly His Arg Asp Thr Leu
345 350

10 TAC ACG ATG CTG ATA AAG TGG GTC AAC AAA ACC GGG CGA 1237
Tyr Thr Met Leu Ile Lys Trp Val Asn Lys Thr Gly Arg
355 360 365

GAT GCC TCT GTC CAC ACC CTG CTG GAT GCC TTG GAG ACG 1276
Asp Ala Ser Val His Thr Leu Leu Asp Ala Leu Glu Thr
370 375

15 CTG GGA GAG AGA CTT GCC AAG CAG AAG ATT GAG GAC CAC 1315
Leu Gly Glu Arg Leu Ala Lys Gln Lys Ile Glu Asp His
380 385 390

20 TTG TTG AGC TCT GGA AAG TTC ATG TAT CTA GAA GGT AAT 1354
Leu Leu Ser Ser Gly Lys Phe Met Tyr Leu Glu Gly Asn
395 400 405

25 GCA GAC TCT GCC WTG TCC TAAGTGTG ATTCTCTTCA GGAAGTGAGA 1400
Ala Asp Ser Ala Xaa Ser
410 411

30 CCTTCCCTGG TTTACCTTTT TTCTGGAAAA AGCCCAACTG GACTCCAGTC 1450
AGTAGGAAAG TGCCACAATT GTCACATGAC CGGTACTGGA AGAAACTCTC 1500

CCATCCAACA TCACCCAGTG GATGGAACAT CCTGTAACCTT TTCACTGCAC 1550

35 TTGGCATTAT TTTTATAAGC TGAATGTGAT AATAAGGACA CTATGGAAAT 1600

GTCTGGATCA TTCCGTTTGT GCGTACTTTG AGATTTGGTT TGGGATGTCA 1650

TTGTTTCAC AGCACTTTT TATCCTAATG TAAATGCTTT ATTTATTTAT 1700

5 TTGGGCTACA TTGTAAGATC CATCTACAAA AAAAAAAAAG AAAAAAAAAG 1750

GGCGGCCGCG ACTCTAGAGT CGACCTGCAG AAGCTTGGCC GCCATGGCC 1799

(2) INFORMATION FOR SEQ ID NO:11:

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(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 411 amino acids
- (B) TYPE: Amino Acid
- (D) TOPOLOGY: Linear

15 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:11:

Met Glu Gln Arg Gly Gln Asn Ala Pro Ala Ala Ser Gly Ala Arg
1 5 10 15

Lys Arg His Gly Pro Gly Pro Arg Glu Ala Arg Gly Ala Arg Pro
20 25 30

Gly Leu Arg Val Pro Lys Thr Leu Val Leu Val Val Ala Ala Val
25 35 40 45

Leu Leu Leu Val Ser Ala Glu Ser Ala Leu Ile Thr Gln Gln Asp
50 55 60

30 Leu Ala Pro Gln Gln Arg Ala Ala Pro Gln Gln Lys Arg Ser Ser
65 70 75

Pro Ser Glu Gly Leu Cys Pro Pro Gly His His Ile Ser Glu Asp
80 85 90

35

Gly Arg Asp Cys Ile Ser Cys Lys Tyr Gly Gln Asp Tyr Ser Thr
95 100 105

His Trp Asn Asp Leu Leu Phe Cys Leu Arg Cys Thr Arg Cys Asp
5 110 115 120

Ser Gly Glu Val Glu Leu Ser Pro Cys Thr Thr Thr Arg Asn Thr
125 130 135

10 Val Cys Gln Cys Glu Glu Gly Thr Phe Arg Glu Glu Asp Ser Pro
140 145 150

Glu Met Cys Arg Lys Cys Arg Thr Gly Cys Pro Arg Gly Met Val
155 160 165

15 Lys Val Gly Asp Cys Thr Pro Trp Ser Asp Ile Glu Cys Val His
170 175 180

Lys Glu Ser Gly Ile Ile Ile Gly Val Thr Val Ala Ala Val Val
20 185 190 195

20 Leu Ile Val Ala Val Phe Val Cys Lys Ser Leu Leu Trp Lys Lys
200 205 210

25 Val Leu Pro Tyr Leu Lys Gly Ile Cys Ser Gly Gly Gly Asp
215 220 225

25 Pro Glu Arg Val Asp Arg Ser Ser Gln Arg Pro Gly Ala Glu Asp
230 235 240

30 Asn Val Leu Asn Glu Ile Val Ser Ile Leu Gln Pro Thr Gln Val
245 250 255

35 Pro Glu Gln Glu Met Glu Val Gln Glu Pro Ala Glu Pro Thr Gly
260 265 270

Val Asn Met Leu Ser Pro Gly Glu Ser Glu His Leu Leu Glu Pro
275 280 285

Ala Glu Ala Glu Arg Ser Gln Arg Arg Arg Leu Leu Val Pro Ala
5 290 295 300

Asn Glu Gly Asp Pro Thr Glu Thr Leu Arg Gln Cys Phe Asp Asp
305 310 315

10 Phe Ala Asp Leu Val Pro Phe Asp Ser Trp Glu Pro Leu Met Arg
320 325 330

Lys Leu Gly Leu Met Asp Asn Glu Ile Lys Val Ala Lys Ala Glu
335 340 345

Ala Ala Gly His Arg Asp Thr Leu Tyr Thr Met Leu Ile Lys Trp
350 355 360

Val Asn Lys Thr Gly Arg Asp Ala Ser Val His Thr Leu Leu Asp
20 365 370 375

Ala Leu Glu Thr Leu Gly Glu Arg Leu Ala Lys Gln Lys Ile Glu
25 380 385 390

Asp His Leu Leu Ser Ser Gly Lys Phe Met Tyr Leu Glu Gly Asn
395 400 405

Ala Asp Ser Ala Xaa Ser
30 410 411

(2) INFORMATION FOR SEQ ID NO:12:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 29 base pairs

35 (B) TYPE: Nucleic Acid

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- (C) STRANDEDNESS: Single
 - (D) TOPOLOGY: Linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:12:

ATCAGGGACT TTCCGCTGGG GACTTTCCG 29

10 (2) INFORMATION FOR SEQ ID NO:13:

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- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 30 base pairs
 - (B) TYPE: Nucleic Acid
 - (C) STRANDEDNESS: Single
 - (D) TOPOLOGY: Linear

20 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:13:

AGGATGGAA GTGTGTGATA TATCCTTGAT 30